

0590
0110

#8

ENTERED



OIPE

RAW SEQUENCE LISTING

DATE: 01/21/2003

PATENT APPLICATION: US/10/006,265

TIME: 16:12:38

Input Set : A:\06501-096001.txt

Output Set: N:\CRF4\01212003\J006265.raw

4 <110> APPLICANT: Maeda, Masatsugu
5 Yaguchi, Noriko
7 <120> TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10
9 <130> FILE REFERENCE: 06501-096001
11 <140> CURRENT APPLICATION NUMBER: US 10/006,265
C--> 12 <141> CURRENT FILING DATE: 2003-01-06
14 <150> PRIOR APPLICATION NUMBER: PCT/JP00/03556
15 <151> PRIOR FILING DATE: 2000-06-01
17 <150> PRIOR APPLICATION NUMBER: JP 11/155797
18 <151> PRIOR FILING DATE: 1999-06-02
20 <150> PRIOR APPLICATION NUMBER: JP 11/217797
21 <151> PRIOR FILING DATE: 1999-07-30
23 <160> NUMBER OF SEQ ID NOS: 40
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2969
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (523)...(2478)
36 <400> SEQUENCE: 1

37	cgcttataaaa tgaatgtgtg cttaggaaca ccagacagca ctccagcact ctgcttgagg	60
38	ggcattcgaa acagcaaaat cactcataaa aggcaaaaaa ttgcaaaaaa aatagtaata	120
39	accagcatgg tactaaatag accatgaaaa gacatgtgtg tgcagtatga aaattgagac	180
40	aggaaggcag agtgtcagct tgttccacct cagctgggaa tgtgcatcag gcaactcaag	240
41	tttttcacca cggcatgtgt ctgtgaatgt ccgcaaaaca ttttaacaat aatgcaatcc	300
42	atttcccagc ataagtgggt aagtgccact ttgacttggg ctgggcttaa aagcacaaga	360
43	aaagctcgca gacaatcaga gtggaaacac tcccacatct tagtgtggat aaattaaagt	420
44	ccagattgtt ctctctgtcc tgacttgtgc tgtgggaggt ggagttgcct ttgatgcaaa	480
45	tcctttgagc cagcagaaca tctgtggaac atcccctgat ac atg aag ctc tct	534
46		
47	Met Lys Leu Ser	
48	1	
49	ccc cag cct tca tgt gtt aac ctg ggg atg atg tgg acc tgg gca ctg	582
50	Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp Thr Trp Ala Leu	
51	5 10 15 20	
53	tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg cca gct	630
54	Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu Pro Ala	
55	25 30 35	
57	aag cct gag aac att tcc tgt gtc tac tat agg aaa aat tta acc	678
58	Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Arg Lys Asn Leu Thr	
59	40 45 50	
61	tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac aca gtt	726

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62	Cys	Thr	Trp	Ser	Pro	Gly	Lys	Glu	Thr	Ser	Tyr	Thr	Gln	Tyr	Thr	Val	
63			55					60					65				
65	aag	aga	act	tac	gct	ttc	gga	gaa	aaa	cat	gat	aat	tgt	aca	acc	aat	774
66	Lys	Arg	Thr	Tyr	Ala	Phe	Gly	Glu	Lys	His	Asp	Asn	Cys	Thr	Thr	Asn	
67			70				75					80					
69	agt	tct	aca	agt	gaa	aat	cgt	gct	tcg	tgc	tct	ttt	ttc	ctt	cca	aga	822
70	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser	Cys	Ser	Phe	Phe	Leu	Pro	Arg	
71	85						90					95				100	
73	ata	acg	atc	cca	gat	aat	tat	acc	att	gag	gtg	gaa	gct	gaa	aat	gga	870
74	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	Ala	Glu	Asn	Gly	
75					105					110				115			
77	gat	ggt	gta	att	aaa	tct	cat	atg	aca	tac	tgg	aga	tta	gag	aac	ata	918
78	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	Leu	Glu	Asn	Ile	
79				120						125				130			
81	gcg	aaa	act	gaa	cca	cct	aag	att	ttc	cgt	gtg	aaa	cca	gtt	ttg	ggc	966
82	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe	Arg	Val	Lys	Pro	Val	Leu	Gly	
83			135					140					145				
85	atc	aaa	cga	atg	att	caa	att	gaa	tgg	ata	aag	cct	gag	ttg	gcg	cct	1014
86	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro	Glu	Leu	Ala	Pro	
87		150					155					160					
89	gtt	tca	tct	gat	tta	aaa	tac	aca	ctt	cga	ttc	agg	aca	gtc	aac	agt	1062
90	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg	Thr	Val	Asn	Ser	
91	165					170					175				180		
93	acc	agc	tgg	atg	gaa	gtc	aac	ttc	gct	aag	aac	cgt	aag	gat	aaa	aac	1110
94	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg	Lys	Asp	Lys	Asn	
95					185					190				195			
97	caa	acg	tac	aac	ctc	acg	ggg	ctg	cag	cct	ttt	aca	gaa	tat	gtc	ata	1158
98	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr	Glu	Tyr	Val	Ile	
99				200						205				210			
101	gct	ctg	cga	tgt	gcg	gtc	aag	gag	tca	aag	ttc	tgg	agt	gac	tgg	agc	1206
102	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp	Ser	Asp	Trp	Ser	
103			215					220					225				
105	caa	gaa	aaa	atg	gga	atg	act	gag	gaa	gaa	gct	cca	tgt	ggc	ctg	gaa	1254
106	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro	Cys	Gly	Leu	Glu	
107			230				235					240					
109	ctg	tgg	aga	gtc	ctg	aaa	cca	gct	gag	gcg	gat	gga	aga	agg	cca	gtg	1302
110	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly	Arg	Arg	Pro	Val	
111	245					250					255				260		
113	cgg	ttg	tta	tgg	aag	aag	gca	aga	gga	gcc	cca	gtc	cta	gag	aaa	aca	1350
114	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	Leu	Glu	Lys	Thr	
115					265					270				275			
117	ctt	ggc	tac	aac	ata	tgg	tac	tat	cca	gaa	agc	aac	act	aac	ctc	aca	1398
118	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn	Thr	Asn	Leu	Thr	
119				280						285				290			
121	gaa	aca	atg	aac	act	act	aac	cag	cag	ctt	gaa	ctg	cat	ctg	gga	ggc	1446
122	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu	His	Leu	Gly	Gly	
123			295					300					305				
125	gag	agc	ttt	tgg	gtg	tct	atg	att	tct	tat	aat	tct	ctt	ggg	aag	tct	1494
126	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser	Leu	Gly	Lys	Ser	

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127	310	315	320	
129	cca	gtg	gcc	acc
130	Pro	Val	Ala	Thr
131	325			
133	tgc	att	gag	gtc
134	Cys	Ile	Glu	Val
135				
137	aag	tgg	caa	agc
138	Lys	Trp	Gln	Ser
139				
141	ttt	ccg	gat	gtg
142	Phe	Pro	Asp	Val
143				
145	tct	cag	gcc	acg
146	Ser	Gln	Ala	Thr
147				
149	tgg	tgc	tat	aac
150	Trp	Cys	Tyr	Asn
151	405			
153	gag	cca	tat	tcc
154	Glu	Pro	Tyr	Ser
155				
157	ggt	cct	gag	acc
158	Gly	Pro	Glu	Thr
159				
161	aca	tgg	aaa	gag
162	Thr	Trp	Lys	Glu
163				
165	tac	acc	atc	ttt
166	Tyr	Thr	Ile	Phe
167				
169	gtc	aat	tcc	agc
170	Val	Asn	Ser	Ser
171	485			
173	acc	tct	tac	att
174	Thr	Ser	Tyr	Ile
175				
177	aac	ggg	acc	agc
178	Asn	Gly	Thr	Ser
179				
181	att	atc	ctc	ata
182	Ile	Ile	Leu	Ile
183				
185	atc	ctg	aca	gtg
186	Ile	Leu	Thr	Val
187				
189	ctg	tgt	tgg	ccc
190	Leu	Cys	Trp	Pro
191	565			

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```

193 tgg cat gga gat gat ttc aag gat aag cta aac ctg aag gag tct gat      2310
194 Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu Lys Glu Ser Asp
195                               585                               590                               595
197 gac tct gtg aac aca gaa gac agg atc tta aaa cca tgt tcc acc ccc      2358
198 Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro Cys Ser Thr Pro
199                               600                               605                               610
201 agt gac aag ttg gtg att gac aag ttg gtg gtg aac ttt ggg aat gtt      2406
202 Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn Phe Gly Asn Val
203                               615                               620                               625
205 ctg caa gaa att ttc aca gat gaa gcc aga acg ggt cag gaa aaa caa      2454
206 Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly Gln Glu Lys Gln
207                               630                               635                               640
209 ttt agg agg gga aaa gaa tgg gac tagaattctg tcttcctgcc caacttcaat      2508
210 Phe Arg Arg Gly Lys Glu Trp Asp
211 645                               650
213 ataagtgtgg actaaatgc gagaaagggtg tcctgtggtc tatgcaaatt agaaaggaca      2568
214 tgcagagttt tccaactagg aagactgaat ctgtggcccc aagagaacca tctccgaaga      2628
215 ctgggtatgt ggtcttttcc acacatggac cacctacgga tgcaatctgt aatgcatgtg      2688
216 catgagaagt ctgttattaa gtagagtgtg aaaacatggt tatggtaata ggaacagctt      2748
217 ttaaaatgct tttgtatttg ggcctttcac acaaaaaagc cataatacca ttttcatgta      2808
218 atgctatact tctatactat tttcatgtaa tactatactt ctatactatt ttcatgtaat      2868
219 actatacttc tatactattt tcatgtaata ctatacttct atattaaagt tttaccct      2928
220 ccaaaaaaag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a
221                               2969
222 <210> SEQ ID NO: 2
223 <211> LENGTH: 652
224 <212> TYPE: PRT
225 <213> ORGANISM: Homo sapiens
227 <400> SEQUENCE: 2
228 Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp
229 1                               5                               10                               15
230 Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala
231                               20                               25                               30
232 Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
233                               35                               40                               45
234 Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
235                               50                               55                               60
236 Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
237 65                               70                               75                               80
238 Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
239                               85                               90                               95
240 Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu
241                               100                              105                              110
242 Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg
243                               115                              120                              125
244 Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys
245                               130                              135                              140
246 Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro
247 145                              150                              155                              160
248 Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg

```

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```

249          165          170          175
250 Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg
251          180          185          190
252 Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr
253          195          200          205
254 Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp
255          210          215          220
256 Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro
257 225          230          235          240
258 Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly
259          245          250          255
260 Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
261          260          265          270
262 Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn
263          275          280          285
264 Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu
265          290          295          300
266 His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser
267 305          310          315          320
268 Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu
269          325          330          335
270 Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp
271          340          345          350
272 Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp
273          355          360          365
274 Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser
275          370          375          380
276 Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys
277 385          390          395          400
278 Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His
279          405          410          415
280 Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly
281          420          425          430
282 Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys
283          435          440          445
284 Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly
285          450          455          460
286 Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly
287 465          470          475          480
288 Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser
289          485          490          495
290 Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Asn Thr Ser
291          500          505          510
292 Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe
293          515          520          525
294 Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu
295          530          535          540
296 Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn
297 545          550          555          560

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; N Pos. 7,8,9
Seq#:22; Xaa Pos. 3
Seq#:26; Xaa Pos. 3,4,5,6,7,8
Seq#:27; Xaa Pos. 3,4,5,6,7,8
Seq#:28; Xaa Pos. 3,4,5,6,7,8
Seq#:34; N Pos. 281,376,420
Seq#:34; Xaa Pos. 24,56
Seq#:35; Xaa Pos. 24,56

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:890 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:894 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:905 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:909 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:910 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:957 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:961 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:26
L:962 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:973 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:977 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:27
L:978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:989 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:993 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:1070 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:1078 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:234
L:1079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:282
L:1086 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:330
L:1087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:378
L:1090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:378
L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:16
L:1113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:48